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                                                                                                                                                       October 1, 1999, 15:34:36 ; Search time 1619.02 Seconds (without alignments) 45.180 Million cell updates/sec
                      GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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| US0733 Human dynam Z75537 Caenorhabdi AJ006304 Bos tauru X93302 S.cerevisia Z49701 S.cerevisia U46154 Sacchoromyc AJ006276 Homo sapi X89068 H. sapiens m Y13758 Homo sapien AC065154 Homo sapien AF111107 Mus muscu AF111107 Mus muscu AF111108 Mus muscu | AF136401 Rattus no U49069 Mus musculu AC00696 Homo saculu X90698 C.erythroce Z80230 Calliphora AC005120 Drosophil AC00614 Drosophil AF08034 Homo sapi Continuation (4 of AL021390 Caenorhabdi L08387 KLebsiella L08387 KLebsiella L08387 KLebsiella U1095 M. lepzae g U99204 Guira g   | PRI 17-OCT-1995  C Msel fragment, clone 164h1,  nt.  ertebrata; Mammalia; Eutheria; ; Homo. inson,P. and Micklem,G. ger Centre, Hinxton, Cambridgeshire, ct: humquery&sanger.ac.uk X. and Bird,A.P. ng a methylated DNA binding column 4)  |
|---|--|--|
| HSU50733<br>CEF18E2<br>BTA6304<br>CSLYS4<br>CSLYS4<br>CSCR419<br>SCG419<br>HSTA6276<br>HSTRF03GN<br>HSTRF03GN<br>HSTRF03117<br>AF093117<br>AF093117<br>AF111107<br>AF111107   | AF136401 MMU49069 AC006969 CETRRHOWO CUTRP AC00514 AC00514 AC005214 AF080394 AF080394 AF080394 AF080390 CEY37H9_3 CEY37H9_3 CEY37H9_3 CEY37H9_3 CEY37H9_3 AC092370 CEY37H9_3 AC092370 CEY37H9_3 AFF10M10 AFF1   | ALIGNMENTS  DNA  NA genomic M  rtla.  el fragment.  cordata, Verte  Hominidae, H  fr.E., Wilkinse  f.E., Wilkinse  f.E., Wilkinse  f.E., Nan,X. e  llands using e  llands using e  llands using e  |
| 1721<br>25321<br>2061<br>30507<br>2716<br>7<br>30507<br>4564<br>10<br>3448<br>11<br>151630<br>11<br>161630<br>11<br>161630<br>11<br>3417<br>11<br>3417<br>11<br>3691<br>12<br>3691<br>12<br>3691<br>12<br>3691<br>12  | 3340 12<br>448 356<br>86667 346<br>129779 376<br>129779 377<br>100000 346<br>110000 346<br>1 | HalfahlR 205 bp H.sapiens CpG island DN Everse read cpg164hl.r. 254791 254791 254791. G:1020832 CpG island; genomic Msehuman. House and cpg164hl.r. 254791. G:1020832 CpG island; genomic Msehuman. House and exarchin; H (bases I to 205) Dodsworth, S.J., Huckle, Direct Submission Submitted (16-007-1995) Cross, S.H., Chariton, J. Purification of CpG isl Nat. Genet. 6 (3), 236-94282070  |
|   | 83 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8   | HS164H1R<br>H.sapiens<br>reverse r<br>254791<br>254791.2<br>254791.1<br>CpG islan<br>human.<br>Homo sapi<br>human.<br>Homo sapi<br>primates;<br>I (bases<br>I (bases<br>CB10 1RQ,<br>CB10 1RQ, |
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Z54791 H.sapiens C

205 9 HS164HlR

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Query Match Length DB

Score 15.8

Result No.

Description

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EQDKFSQARAKVAELERTALTACCDQAQNPLSAGLGGACLMETVELLQAKVSALL
DLAVLDQVEARLQALGKVNETERHASVEDADTOSKVHOLYETIQHWSPTASTLPEL
VQRLYTIKQLHEQAMOFGQLLTHLDTTQOMIANSLKDNTTLLTQVQTTMRENLATVEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1721)
Echeverric,CJ, Paschal,B.M., Vaughan,K.T. and Vallee,R.B.
Molecular characterization of the 50-kD subunit of dynactin reveals function for the complex in chromosome alignment and spindle organization during mitosis

96178072
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Clones are available from the UK MRC Human Genome Mapping Project Resource Centre, Hinxton, Cambridgeshire CB10 1RQ, UK. See URL: http://www.hgmp.mrc.ac.uk/ for details or contact. blohelp@hgmp.mrc.ac.uk.

Location/Qualifiers

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Direct Submission

Submitted (05-MAR-1996) Christophe J. Echeverri, Cell Biology,
Worcester Foundation for Biomedical Research, 222 Maple Avenue,
Shrewsbury, MA 01545, USA

Location/Qualifiers
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ilarity 63.6%; Pred. No. 3.4e+02;
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                                                                                                                                                                                                                             /clone="164h1"
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Echeverri, C.J.
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L Submitted (29-JUN-1996) Louis, MO 63110, USA. E-mail:
Submitted (29-JUN-1996) Louis, MO 63110, USA. E-mail:
Jebses 1 to 25321)
Signification of rw@nematode.wustl.edu
E 2 (bases 1 to 25321)
Signification of rw@nematode.wustl.edu
E 2 (bases 1 to 25321)
Sonfield, J. Burton, J., Connell, M., Copsey, T., Cooper, J.,
Bonfield, J., Burton, J., Craxton, M., Dear, S., Durbin, R., Favello, A.,
Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M.,
Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N.,
Latreille, P., Lighthing, J., Lloyd, C., McMurray, A., Mortimore, B.,
Callaghan, M., Parsons, J., Percy, C., Rifken, L., Sonnhammer, E.,
Staden, R., Sulston, J., Thierry Mieg, J., Thomas, K., Vaudin, M.,
Waughan, K., Waterston, R., Waterston, R., Weinstock, L.,
Wilkinson-Sproat, J. and Wollidman, P.,
St. Mo of contiguous nucleotide sequence from chromosome III of C.
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IMPORTANT: This sequence is not the entire insert of clone F18E2. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone F18E2 is at 1 in this sequence. The true right end of clone E18E2 is at 14886 in sequence 275554.

The true left end of clone 2C455 is at 25221 in this sequence. The true right end of clone 2C455 is at 24380 in this sequence. The strue right end of clone 2C455 is at 24380 in this sequence. The structure right end of clone 2C455 is at 24380 in this sequence. The structure right end of clone 2C455 is at 24380 in this sequence. The structure right end of clone 2C455 is at 24380 in this sequence. The
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bin/display?db=wormace&class=Sequence &object=F18EZ
current sequence finishing criteria for the C. elegans genome
sequencing consortium are that all bases are either sequenced
unambiguously on both strands, or on a single strand with both a
dye primer and dye terminator reaction, from distinct subclones.
Exceptions are indicated by an explicit note.
Exceptions are indicated by an explicit note.
This sequence is NOT necessarily the entire insert of
the specified clone. It may be shorter because we only sequence
overlapping sections once, or longer because we arrange for a small
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 25321)
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   Length 1721;
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                                                                              Indels
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Score 15.8; DB 11;
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Nature 368 (6466), 32-38 (1994)
                                                                                                                                                                                                Db 1244 CAGTTGAGGGAACTTTGCCAG 1265
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       68.78;
63.68;
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Direct Submission
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           Query Match
Best Local Simi
Matches 14;
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EFLFDGKRVFFSIALIYTYGTLVSNFSPSIIENSALMAMIADPLTIDPEYKUDEITDW
KRYHYQGYNWAIFONAFIKALIYTYGTLYSPSIIENSALMAMIADPLTIDPEYKUDEITDW
MSYNALMAFVVPANYTALAELCWSIVHGCPALIYLTMNYTRIFFLKFLKIKKTINKVN
NATSRSNMNTSKSNFL
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/note="Similarity to Drosophila Guanine nucleotide-binding
protein (SW:GB01_DROME)"
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QQEKIEVMHKMRQHVAQYAKLIIHGAMPVAEASHLIKRYQSHFQDFGDIFKNLLSKCR
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AISSLHKKAIDFAFEEYDKENHQMPKNIFFLEIAIEFSGKLLAQDKMAVVRYLNKIYT
NRVGTSTVVWEPYRLYLGSLSDRNDDDNMSVRSGMTVTSNAIMRSTASSTRGRGRG
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                                                                                                                                                                                                                                                                                                                                                                     DVRERSMOMLFMOLCFDSMNIKKEGETPKADOVRKLKKRRDOLIRIVTETLNEEACGV
EMBL:D67647 comes from this gene; cDNA EST yk448f1.3 comes from this gene; cDNA EST yk448f1.5 comes from this gene; cDNA EST yk260g1.3 comes from this gene; cDNA EST yk260g1.5 comes from this gene; cDNA EST pk280g1.5 comes from this gene; cDNA EST yk28cg2 from this gene; cDNA EST yk27e9.5 comes from this gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Join (complement (1233. .1262), complement (816. .909), complement (578. .762), complement (46. .200), complement (578. .762), complement (46. .200), complement (27527.1:20448. .20576), complement (27527.1:20448. .20576), complement (27527.1:2063. .20216), complement (27527.1:19840. .19976), complement (27527.1:19840. .19976), complement (27527.1:19578. .19674), gene="gpa-13" .1262), complement (816. .909), complement (578. .762), complement (27527.1:20448. .20576), complement (27527.1:20468. .2032), complement (27527.1:2063. .2032), complement (27527.1:2063. .20316), complement (27527.1:2063. .20316), complement (27527.1:19840. .19976), complement (27527.1:19578. .19634))
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Pred. No. 2.2e+02;
4; Mismatches 4;
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Best Local Similarity 63.6%;
Matches 14; Conservative
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/ AD xref="PID: 61345819"

/ AD xref="PID: 61345819"

/ AD xref="PID: 613456095"

/ AD xref="PID: 613456095"

/ AD xref="STREMBL: 013954"

/ AD XRED STREMED STREME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(4069. .4165,4214. .4473,4519. .4653,
4702. .4812,4962. .5192,5250. .5497,5794. .5937,5988. .6129))
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[2568. .13757,13812. .14040)
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IGPVHWVGVSTETYGYYYEZGMDPVMTQYDMLKRDLTTANSNRAAHPMIFTFQHRFY
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WNDPNAYINPKAPVYLISGSAGCHTPDALFTDKPWPWSAARNNDYGWSIVTVANRTHI
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GLAAHAHTVKIKDLSGGGKSRVALCNLALGGPDIIILDEPTNNLDIESIDALAEAIRD
FNGGVYWYTHDERLYVRTDCNLMYVENQGIDEIDGDFEDYKKEVLDALGEALVSKK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Similarity to Aspergillus acid phosphatase (TR:G755244)"
                                                                                                                         /organism="Caenorhabditis elegans"
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complement(4069. .6129)
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1. .25321
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TDAAAIWATGOTWWOIPPYAOYELKGOLPQGYSGKDIIYALCGLFNNDOYLHHAIEFT
GDSLNALPIDHRLTIANMTTEWGALSGLFPUDKTLIDWYKNRLQKLGTNNHFRINPKT
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REKYQGARKEITRRTGWFLKMDVADAKVVYTEGSLDGPVILEOKVGELGKNLQEIIVK
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                                                                                                                                                                                 Direct Submission Submission Submitted (27-NOV-1995) F. Gamonet, IBGC-CNRS, CNRS, 1, rue Camille Sabmitted (27-NOV-1995) F. Gamonet, FRANCE Saint Saens, F-33077 Bordeaux Cedex, FRANCE Location/Qualifiers
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       Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales; Saccharomyeetaceae; Saccharomyces.

1 (bases 1 to 2716)
Gamonet, F. and Lauquin, J.M.
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277. .2358
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65.2%; Pred. No. 3.4e+02;
iive 3; Mismatches 5;
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S.cerevisiae chromosome IV cosmid 8419.
249701 271256
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/db_xref="SGD:S0002642"
558 c 587 q 75
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337. .2355
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Saccharomyces cerevisiae
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/gene="lys4"
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                                                                                                              Unpublished
2 (bases 1 to 2716)
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RRPGGASYLSRYTTRYNRSPQNIGPPTPETTATVSRUGSSEIGLPPDAGGAQA

PASGESGPSSPAHTLUNREQESEGAGDLPQEADLGAKEGT"
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Submitted (19-MAY-1998) Wissenbach U., Universitat des Saarlandes,
Submitted (19-MAY-1998) Wissenbach U., Universitat des Saarlandes,
Pharmakologie und Toxikologie, D-66421 Homburg, Saarland, GERMANY
(bases 1 to 2061)
Wissenbach, U., Schroth, G., Philipp, S. and Flockerzi, V.

Missenbach, U., Schroth, G., Philipp, S. and Flockerzi, V.

Massenbach, U., Schroth, G., Philipp, S. and Flockerzi, V.

Massenbach, U., Schroth, G., Philipp, S. and Flockerzi, V.

FEBS Lett. 429 (1), 61-66 (1998)
                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Artiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bosinae; Bos.
1 (bases 1 to 2061)
Wissenbach, U.
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65.2%; Pred. No. 3.5e+02;
Live 3; Mismatches 5; Indels 0.
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AJ006304.1 GI:3152951
TRP-related; TRP2 gene; Trp2 protein.
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                                                                                                                             BOS taurus mRNA for TRP2 protein.
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1. 2061
Corganism="Bos taurus"
Ab_Xref="taxon:9913"
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X93502.1 GI:1089839
homoaconitase; Lys4 gene.
    codon_start=1
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613. .1911
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GQELSVETRRDGRIVYXNXGQYLSBANDDLSVLPMYLSVGKNPFYGNDFKTHEHIH
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LOLOQITGCRPHPITESKNDVPTWKLRKGHOMGAKVELKGKEMSOFLSTLTEIVLPRIF
EYKGISNQSGNRFGGISFGLTAEDIKFFPEIDANQDSWPKTFGMHININTSAOLDYQA
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KSILVTWIEGGRAPPELLMHITRFYMSKNKELKKLLYFYWEIVPKLAEDGKLRHEMIL
VCNAIGHDLQHPNEYIEGHTRFYLKTKREAELLEDOWPSVLACLEYBHAYTRKYAILA
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LDVRSKALDISMULATSSNAIGHTYUDRKQDINRNNYAGALESTLDLIKHLAED
LDVRSKALDISMULATSSNAIGHTYUDRKQDAAAASHESTLDLIKKTRAED
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NNFVEMAASVVSLLLDFIGDLNSVAASGIIAFIKEVIEKYPOLRANILENNYQTLDKY
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NNFVEMAASVVSLLLDFIGDLNSVAANGINTANICHENTY
DIVEFVEKNIFOKIIEFGWEYYLQNGMFWNCYCRLIYFDISRSYLDKRQYIVRKIWPQ
IDKKFAQSYLFSLTEFCESYFPEEMDTLEEMFTEEF"
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KRFYTVTWKSSADTGVIFGNIIVDGAHGEDARYVILMDVHVDTMDYTRFATADDEHF
RTMRNAFERENKISKSQLPFLHALLRELNKGTNMGIITPSESLGEDDCRFLSCNLYA
KSSFGEDALANLCIEKDSKTNDVIGYVRIRSKGQGLALSLGBRYALIAKKTNKLALTH
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TSISILLDEVNPEEKKEEVKLLEVAFLDTIKSSFKRQIEIAKKNKHKRALKDSCKNIE
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NIARTSTAETSAPDIPPRSPNRNAHSRSHSIQAPLQKETLKNTNPFLNAEDTLGDSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4533. .5411
/note="YD8419.04, len; 292, CAI: 0.16, C-terminal similar
to 508 ribosomal protein L5"
/codon_start=1
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/note="YD8419.06c, unknown, len: 787, CAI: 0.12, potential
coiled-coil region"
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/db_xref="G1:817824"
/db_xref="SWISS-PROT:p41810"
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/db_xref="SGD:S0002646"
complement(5813. .8734)
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                                                               complement(3154.
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Barrell, B. and Rajandream, M.A.
Direct Submission
Submitted (20-MX-1995) Saccharomyces cerevisiae chromosome IV
sequencing project, Sanger Centre, Hinxton Hall, Hinxton, Cambridge
CB10 IRQ E-mail: barrell@sanger.ac.uk
                                   AMDY; amidase; coatomer; dehydratase; delta element; gluconokinase;
PAMI; protein kinase; PRP28; ribosomal protein; SEC26; sigma
element; SUP2; transfer RNA-Tyr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                All CDS over 100 codons have been analysed. CDS that are completely overlapped and those that are overlapped by more than 50% of their length by a larger CDS have been omitted from this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORSILLMTSYLKFCNNVISHOKQLFKKYETAEEVYGLHFFSGEFWINTENSSRCTS
SKKYNNVLRILEIPLHSFSKFYALMLORIDDIMDLKQLSQLTSKDELLKKLKIDINY
SKKYNNVLRILLEIPLHSFSKFYALMLORIDDIMDLKQLSQLTSKDELLKKLKIDINY
SKRKGPYLQDAKKKLKKITREMYMYQYQYGLEISISIFESKIYINYYFSFETLYSSDEI
ETWIKYLDYTITLGTDSLTHLNFQRALLPLHYDLWIKYSKRIINSKNDLLGARNVL
LMGLKFSLKKTEIIKLLSVICKLNEYVLKRALEKTESSYSDNVENVDFFETFWDYL
QFKTFCQNSLYSSRYSDSQSNGLLNKELFDKVWKRLSCKEKKSGQEILLNNLVQFYSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TEIIENPVVEEEVNAQTEAPKQSVEILEGEPREFSGEIVLCDADNINTDGIYPOKYTY
QDDVPKEKMAQVCMENYDAEFRIKVHPGDIVVSGFNFGTGSSREQAATALLAKGINLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="SNTVQDLSQQDIKINKAYLVSCTNSRLSDLQSAADVVCPTGDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVNKVAPGVEFTVAAASSEIEADARKSGAWEKLLKAGCIPLPSGCGPCIGLGAGLLEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <1. 1128
/oote="YD8419.01, putative dehydratase, incomplete orf -
overlaps orf YD9934.18, len: > 375, CAI: 0.23, similar to
3-isopropylmalate dehydratase and aconitate dehydratase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEVGISATNRNFKGRMGSKDALAYLASPAVVAASAVLGKISSPAEVLSTSEIPFSGVK
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                                                                                                                                                                         Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
1 (bases 1 to 30507)
Oliver,K. and Harris,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Details of the omitted CDS are available on request. The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons and the calculated codon adaptation index (CAI) is given for each CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="overlap with cosmid 9934, EMBL ID SC9934"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1422. .3056
/note="YD8419.02, unknown, len: 544, CAI: 0.14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VVTEGSLDGPVILEQKVGELGKNLQEIIVKGGLEGWVKSQL"
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/db_xref="GI:817821"
/db_xref="SPTREMBL:Q03776"
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/protein_id="CAA89720.1"
/db_xref="PID:9817820"
/db_xref="GI:817820"
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/chromosome="IV"
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1. .30507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
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              GI:817819
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                                                                                                                                         baker's yeast.
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JOURNAL
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
   VERSION
KEYWORDS
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/translation="MLRSTTETRSFHSSRAWIKGQNLTEKIVOSTAVNLDEGKVVHSG
DYSSIRPAHONSHDNSWPVALKEWGIGATKIKNBSOLYTTLDHDIONSESKNITKYKN
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TDAAAIWATGOTWWADIPPVAQVELKGOLPQOYSGKDIIVALCGLFNNDOVLNHAIEFT
GDSLANLPIDDRLTIANMTTENGALSGLFPVOKTLIDWYRKLOKLGTNNHPRINFY
IRALEEKAKIPKADKDAHYAKKLIIDLATLTHYVSGPNSVKVSNTVODLSQODIKINK
AYLVSCTNSRLSDLOGAADVVOPTGDLNKVNKNAPGYBEYVAAASSELEADARKSGAM
EKLLKAGCIPLPSGGGFGIGLGAGILEPGEVOISATNNHFNNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VAASAVLGKISSPAEVLSTSEIPFSGVKTEITENPVVEEEVNAQTEAPKQSVEILEGF
PREFEGELUKCDADNINTDGITPGKTYTQDVPKEKNAQVCKENYDADAFERTKVHEGDI
VVSGFNFGTGSSREGAATALLAKGINLVSGSFGNIFSRNSINNALLTLEIPBLIKKL
REKTQGAPKELTRRGWFLKNDVADAKVVVTEGSLDGPVILEGKKUGELGKNLQEIJVK
                                                                                                                                                               2 (bases 1 to 2710)
Irvin, S.D. and Bhattacharjee, J.K.
A unique fungal lysine biosynthesis enzyme shares a common ancestor
with tricarboxylic acid cycle and leucine biosynthetic enzymes
                                     Wang, L., Okamoto, S. and Bhattacharjee, J.K. Cloning and physical characterization of linked lysine genes (lys4, lys15) of Saccharomyces cerevisiae Curr. Genet. 16 (1), 7-12 (1989) 90003361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="genomic library of S. Okamoto (1983), Abstr. Met. Mol. Biol. yeast, Cold Spring Harbor laboratory, NY, p. 29" <276. .>2357
                                                                                                                                                                                                                                                                                                                               (asses 1 to 2710)
Irvin, S.D. and Bhattacharjee, J.K.
Direct Submission
Submitted (17-Jan-1996) Jnanendra K. Bhattacharjee, Microbiology,
Miami University, 32 Pearson Hall, Oxford, OH 45056, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="lysine biosynthesis enzyme homoaconitase"
/db_xref="5GD:S0002642"
<276. ,>2357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product-"lysine blosynthesis enzyme homoaconitase"
/protein_id="AAA88902.1"
/db_xref="PiD:g1197581"
/db_xref="GI:1197581"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Saccharomyces cerevisiae"
/db_xref="taxon:4932"
/chromosome="IV"
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/note="cis-homoaconitate hydratase"
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J Mol. Evol. 46 (4), 401-408 (1998)
98210230
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Saccharomycetaceae; Saccharomyces
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65.2%;
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/qene="LYS4"
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Best Local Similarity 65.2
Matches 15; Conservative
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MEDLINE
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AUTHORS
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HSAJ6276
LOCUS
                                               AUTHORS
TITLE
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AKSNESSQSGLSISKGSKSTVLAALDSNGNTKSSNKTSELNSINSISESLYPAAHSFN
AKSNESSQSGLSISKGSKSTVLAALDSNGNTKSSNKTSELNSINSISESLYPAAHSFN
TSNFLOAPPULPVAKGNNULIOPKSTROKSPLTSSKOLGIKHGKVKOKLLALETRNEE
SDGTAATCLKNKINVDHTKEFHKLLGKENETGSISKKEGTDAEQAEDYLKDIPGDEAIN
LODPRDANARNISROGSYDSYSTSNTVSSYTRSQNRARSGTLDNDYNNRQKLPTHIS
LODPRDANARNISROSYSTNSTVDVDLSYSTGHGLRVANPDSDFF"
complement(11592. 13070)
/note="YD8419.07c, unknown, len: 492, CAI: 0.13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDIWKNLDRIRSTKKNAGQFIKGSLLILPMRTEDKQQFDECMDELHKYISKDILRCYP
QKEQKDEGMLFYIVLKDFNILDSCFVLSVLLAFQKRLWMAPSEKSYFRVPKNINLTGS
FYLPRNIETGRGHITSYRREQPSSSTVGVGFWVDPDQGGGVKACHVSKFWNELSNF
FSQVEFGCAGNVINYFKFWNRTSQSJSLALYELPLIGDGLEDIKSYISKTRFILET
SKAQMIKHISEMKATREISGLQGDQFPRQQRPLSNSPSSNSISSSQTIEAGATSYQTO
PQRHAVNKPSNVLNSSNRHSGPKTFEDGRYSEGNKFQFMTQDEIKQHCIGTIKASMDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="wiliffAyisrretvsQRQTSTIVYNITLMFSTLRCALKILAQI
KKRLQQTSSNHENKKYEEVIKDHVGVKIQNIICLLAFVLVVYYQMRCKKMT"
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KSNEHLGSDGSIASARKPLRITNEIDSGSSNEDDDDGLQEKGFVDSESKAFINYASDQ
  LTOSKEASGNDHKGIEYLQENNIIGQRTNPFTTSANSNAHFSKIKRSRPPPPPMDMKS
ITTSISNNTTKEEIESNNDSERDSIAISSTHNQHRRQRSEAEKLVDDIENYINEHKVS
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Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
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67.8%; Score 15.6; DB 7; Length 30507;
Best Local Similarity 65.2%; Pred. No. 2.7e+02;
Matches 15; Conservative 3; Mismatches 5; Indels 0;
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complement(13873. .14213)
/note="solo sigma element"
14230. .14318
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/db_xref="GI:817827"
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/db_xref="PID:9817826"
/db_xref="GI:817826"
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/gene="AMDY"
/db_xref="SGD:S0002650"
14725. .16374
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Score 15.6; DB 10;
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Cell 89 (7), 1155-1164 (1997)
97358541
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/gene="trpc3"
<1. .>353
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Best Local Similarity 65.2%;
Matches 15; Conservative 3
                                      x89068.1 GI:1019789
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Montell, C.
                                                             TRPC3 gene.
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                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukheria: Primates; Catarrhini; Hominidae; Bomo.

1. (bases 1 to 4564)

D'Esposito, M., Strazzullo, M., Cuccurese, M., Spalluto, C., Rocchi, M., D'Urso, M. and Ciccodicola, A.

Identification and assignment of the human transient receptor potential channel 6 gene TRPC6 to chromosome 11q21-->q22

Cytogenet. Cell Genet. 83 (1-2), 46-47 (1998)
Homo sapiens mRNA for transient receptor potential protein TRP6.
AJ006276
                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission Submission Submitted (18-70W-1998) International Institute of Genetics and Biophysics, Via Marconi, 10, Napoli 80125, ITALY Location/Qualifiers 1, 4564
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Pred. No. 3.2e+02;
3; Mismatches 5; Indels 0;
                                                                                 AJ006276.1 GI:4454260
transient receptor potential protein; trp6 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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/map="q21-22"
428. 3223
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H.sapiens mRNA for TRPC3 protein.
X89068
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/evidence=experimental
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/gene="TRP6"
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Best Local Similarity 65.2%;
Matches 15; Conservative
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/gene="TRP6"
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/codon_start=3
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/db_xxef="GI:1019790"
/db_xxef="SPTREMBL:015660"
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EIEDDSDVEWKRARSKLWLSYFDDGKTLPPPFSLVPSPKSFVYFIMRLVNFPKCRRRR
LQKDIGNGEWGNSKS"
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                                                                                                                                                                                                                                                                                                                        Direct Submission

Submitted (106-1011-1995) C. Montell, The Johns Hopkins Univ. School of Model (106-1011-1995) C. Montell, The Johns Hopkins Univ. School of Model. Dept of Biological Chemistry, 725 N. Wolfe Street, Baltimore MD 21218, USA

Related sequence R34716.

Location/Qualifiers

1. 353

1. 353

Abstract Homo sapiens"

/db_xref="taxon:9606"
/dev_stage="fetal"
Homomogapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 353)
Wes, P.D., Chevesich, J., Jeromin, A., Rosenberg, C., Stetten, G. and Montell, C.
Montell, C.
TFPC1, a human homolog of a Drosophila store-operated channel
Proc. Natl. Acad. Sci. U.S.A. 92 (21), 9652-9656 (1995)
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3448)
Xu,X.Z., Li,H.S., Guggino,W.B. and Montell,C.
Coassembly of TRP and TRPL produces a distinct store-operated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="transient receptor potential channel related"
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transient receptor potential channel; TRPC3 gene.
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us-09-026-400-5.rge

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DAABEGON POWREMLEESTINGERAAGKRILLESPERDELEODDEPTAYDEDCHRESPD
ITP ILLAAHGOKYEVUHMILMGARIERPHDYFCKGEDOMEGAHDSFSHERSPINAY
KGLASPAYLSISSEDPYLTALELSNEIRPHDYFCKGEDOMEGAHDSFSHERSRINAY
KGLASPAYLSISSEDPYLTALELSNEIRAALANIEKEEKNDYRKLENGCKDEVVGVULDY
CRDSBEVERA ILNGDLESAEPLEVHRIKASISRYKLAIKEVKEYKRYPHPHOCOOLLTW
YENLSGLEROTIALIKULVVLVVALGLEPIALIGYNIAPCSRIGKILRSPFNKEVAHAAS
FIIFLGLLVFNRABRFEGTTLENTVTDYPROLIFRYKTTOFTWEMILNWWVLGMM
SECKELWLEGPREY ILOLMVLDFGMLSIFTARFLEACHARGOYVDSYVQES
DLSEVTLEPPEIQYFTARDWHLPSDPQIISEGLYAIAVLSFSRIAYILPANESFGPL
OISLGRTVKDFRKEWLEINGYLZOYLYGITNVTWYVLIMLIALINSSYOEIEDDSD
VEMKFARSKALLSFENDGKTLEPPESHSFUNDFKSEYVYTHMINSYVELED
VEMKFARSKALLSFENDGKTLEPPESHSFUNDFKSEYVYTHMINSYVENDE
VEMKFARSKALLSFENDGKTLEPPESHSFUNDFRYKSYVYRTHMINSYVENDE
VNEGELKEINDFTOSNSRYFESHSELNEPPERALIHKLSKRYYLKRRYYLKAROYDKENDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence. AC005154
                                                                                                                                                                                                                                                                                                              /product="transient receptor potential related channel 3
Montell,C.
Direct Submission
Direct Submission
Submitted (12-JUN-1997) C. Montell, The Johns Hopkins University
School of Medicine, Department of Biological Chermistry, 725 N.
Wolfe Street, Baltimore, MD 21205, USA
Related sequences: X89068, U47050.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Bauer,C., Langston,Y. and Harrison,M.
The sequence of Homo sapiens PAC clone DJ0777023
Unpublished (1998)
2 (bases 1 to 151630)
Waterston,R.
                                                                                                                                                1. 3448

Organism="Homo sapiens"

/db_xref="taxon:9606"

425. 2971

425. 2971

/gene="TRPC3"

/gene="TRPC3"
                                                                                                                                 Location/Qualifiers
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Best Local Similarity 65.2
Matches 15; Conservative
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MAPPING INFORMATION:
The sequence of this clone was established as part of a mapping and sequence of this clone between the NHGRI Chromosome 7 Mapping sequencing collaboration between the NHGRI Chromosome 7 Mapping sequencing collaboration by Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc
                                                                                                                                                               NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                              This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate commistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone was derived from human PAC library RPCI-4, prepared by Pieter de Jong and coworkers at Roswell Park Cancer Institute, using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from one male donor. For further details, see http://bacpac.med.buffalo.edu/
The clone is available from Genome Systems, Inc.
(http://www.genomesystems.com).
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The actual start of this clone is at base position 1 of DJ0777023;
actual end is at 151630 of DJ0777023.
Location/Qualifiers
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3771. .4076
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                                                                                                                      mailto:sapiens@watson.wustl.edu
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/rpt_family="L1"
5266. Feef
Department of Genetics Washington University St. Louis MO 63108, USA http://genome.wustl.edu/gsc
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Muman:

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria: Primates; Catarrhini; Hominidae; Homo.

Eutheria: Primates; Catarrhini; Hominidae; Homo.

Eutheria: Primates; Catarrhini; Hominidae; Homo.

E 1 (Dases 1 to 147216)

S Blechschmidt,K., Nordsiek,G., Drescher,B., Weber,J., Schattevoy,R., Korenberg,J. and Rosenthal.A.

Direct Submission

Location/Qualifiers

1. 147216

Actional Small Memo sapiens"

Abox ref="taxon:9606"

Abox ref="taxon:9606"

Abox ref="taxon:9606"

Actional Taxon:9606"

Actional Taxon:9606"

Actional Family="MAR"

Actional Family="MAR"

Actional Complement(427. .480)

Arpt_family="MAR"

Actional Complement(481. .739)

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47168. .47308))
//gene="Waldsca:H_DJ0777023.1"
//note="Similar to protein U28928 (PID:g861306);
H_DJ0777023.1"
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Homo sapiens chromosome 7qtelo BAC E3, complete sequence.
AF093117
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VEWKRARKLAKLSTEDMIGTORFYVESHSRFNSHLAMINSSYQEREDDSD
VEWKRARKLAKLSTEDMIGTORFYNSHRELAILHKLSEKLARRYLKAQVDKENDE
VNEGELKEIRODISSLRRSENSHILHHKLSEKLARRYLKRYVLKAQVDKENDE
VNEGELKEIRODISSLRSELEDMIGTORFYNSHLERILIHKLSEKLARRYLKEST
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutherla, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 2842)
Buess, M., Engler, O., Hirsch, H.H. and Moroni, C.
Search for oncogenic regulators in an autocrine tumor model using differential display PCR: Identification of novel candidate genes including the calcium channel mtrp 6
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Mus musculus putative capacitative calcium entry channel (Trp6)
mRNA, complete cds.
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1. .2842
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AF057748.1 GI:3766190
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22. .2652
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LOCUS
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KEYWORDS
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call 85 (5), 661-671 (1996)
96234226
2 (bases I to 3417)
2 hu, X., Peyton, M. and Birnbaumer, L.
Direct Submission
Submitted (24-JaN-1996) Xi Zhu, Anesthesiology, UCLA School of Medicine, BH-612, CHS, Los Angeles, CA 90095-1778, USA
On Aug 4, 1997 this sequence version replaced gi:1326112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSU47050 3417 bp mRNA PRI 04-AUG-1997
Human putative calcium influx channel (htrp3) mRNA, complete cds.
U47050
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhin1; Hominidae; Homo.

1 (bases 1 to 3417)
Zhu,X., Jiang,M., Peyton,M., Boulay,G., Hurst,R., Stefan1,E. and
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65.2%; Pred. No. 2.3e+02;
Live 3; Mismatches 5; Indels 0;
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40146. 40573

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    /db_xref="taxon:9606"

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U47050.1 GI:2295902
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Best Local Similarity 65.29
Matches 15; Conservative
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                                                      repeat_region
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OODAEWNKRNEEKKFSYFBEGGRTLDVPPNLVPSPKSLIYLLKEKKWCELIOGOKOGF
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Butaryotas, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butharyota; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 3691)
1 (bases 1 to 3691)
2 (bases 2 to 3691)
3 (bases 2 to 3691)
3 (bases 2 to 3691)
3 (bases 3 to 3691)
3 (color at 36
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INAYKGLASPAYLSLSSEDPVMTALELSNELAVLANIEKEFKNDYRKLSMQCKDFVVG
LSRVGDALLLAISKGYVRIVEAILNHPAFAEGKRLATSPSQSELQQDDFYAYDEDGTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF111107 3691 bp mRNA ROD 15-MAR-1999
Mus musculus transient receptor potential 2 (Trp2) mRNA, complete
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2 (bases 1 to 3691)
Direct Submission
Submitted (04-DEC-1998) Anesthesiology, UCLA, 10833 Le Conte Avenue, Los Angeles, CA 90095-1778, USA
Location/Qualifiers
1. 3691
/ Organism="Mus musculus"
/ Ab.xref="taxon:10090"
/ Lissue_type="testis"
1. 3691
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Pred. No. 3.4e+02;
3; Mismatches 5;
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2071 GACGTGGAGTTGGAAGTTTGCAAG 2093
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AF111107
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Title:

US-09-026-400-5 23

1 gcngtngartggaayttygcnmg 23 Perfect score: Sequence:

311585 seqs, 125096042 residues IDENTITY\_NUC Scoring table: Searched:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | cription      |      | Nicotianamine amin | Nicotianamine amin | transient re | =     | Streptococcus pneu | -      | uncoupling p | uncoupling p | uncoupling p | ы     | coupling | e of the |         | la tenella sp | Microspore-specifi | ₽    |       |       | na       | napus m  | ŝ     |      | Ŋ    | ß    | S    | ທ    | S    | o.   | ທ    | ທ    | ťΩ   | ha     |       | almonella enteric | йd   | long unique c | LUR DNA (nucl | Nucleotide sequenc | C10-16 DNA fragmen | ť     | iana tabacum | roxid |
|-----------|---------------|------|--------------------|--------------------|--------------|-------|--------------------|--------|--------------|--------------|--------------|-------|----------|----------|---------|---------------|--------------------|------|-------|-------|----------|----------|-------|------|------|------|------|------|------|------|------|------|------|--------|-------|-------------------|------|---------------|---------------|--------------------|--------------------|-------|--------------|-------|
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| SUMMARIES | Δ             | 7    | 0                  | m                  | 0            | 8     |                    | O.     |              |              |              |       |          |          |         |               |                    |      |       |       |          |          |       |      |      |      |      |      |      |      |      |      |      |        |       |                   |      | #1 K          |               |                    |                    |       |              |       |
| Š         | ID            | V481 | ന                  | V481               | n            | V2603 | V5224              | V54602 | V717         | V717         | V726         | V726  | V84254   | N925     | T935    | T935          | 0057               | 0057 | 0468  | 0997  | T488     | T488     | V260  | T731 | T731 | T731 | T731 | T731 | T731 | T/31 | T731 | 1/31 | 1/31 | V579   | V579  | X067              | T894 | V199          | V738          | X268               | 0206               | 0253  | 0294         | 0315  |
|           | DB            | !    |                    |                    |              |       |                    |        |              |              |              |       | Η.       |          |         |               |                    |      |       |       |          |          |       |      |      |      |      |      |      |      |      |      |      |        |       |                   |      |               |               |                    |                    |       |              |       |
|           | Length        | 1660 | 23                 | 1910               | 3258         | 29    | 11303              | 1193   | 1220         | 1033         | 1231         | 1132  | 2340     | 3094     | 2997    | 3094          | 4976               | 1938 | 29879 | 1054  | 4977     | 1938     | 3290  | 1344 | 1441 | 1417 | 1395 | 1374 | 1366 | 1412 | 1350 | 1347 | •    | 237326 | ന     | 22080             |      | 137507        | 35100         | 9626               | 855                | 5270  | 1812         | 1918  |
| оF        | Query         | 80.0 |                    |                    |              |       |                    |        |              |              |              |       | 64.3     |          |         |               |                    |      |       |       |          |          |       |      |      |      |      |      |      |      | 61.7 |      |      |        |       |                   |      |               |               |                    |                    |       |              |       |
|           | Score         | 18.  | œ.                 | 7.                 | 'n.          | 2     | S.                 | 4      | 4            | 4.           | 4            | 4.    | 14.8     | 4        | 4.      | 4.            | 4                  | 4    | 4     | 4     | 4        | 4        | 4     | 4    | 4    | 4.   | 4    | 4.   | 4.   | 4.   | 4.   | 4.   | 4.   | 4      | 4     | ಶ                 | 14   |               | 14            | ٦                  | m                  | 13.6  | m            | 'n    |
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EP-860499-A2. 26-AUG-1998. 19-FEB-1998; 102891. 21-FEB-1997; JP-037499.

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Claim 4; Page 12-13; 17pp; English.
The nicotianamine aminotransferase can be used in a plasmid to transform plant cells to produce cells with enhanced iron absorption, and it is implied [though not stated] that plants with improved resistance to iron deficiency chlorosis in calcareous soils can be regenerated from the transformed cells. The gene fragment can be used to detect, amplify and/or isolate nicotianamine aminotransfess genes. 365 T; sequence 1660 BP; 423 A; 442 C; 430 G; 355 T;
Human brain Expres
Superoxide dismuta
                                                                                                                                                                                                                                                                                                          7.007-1998 (first entry)
Nicotianamine aminotransferase 49564.15 molecular weight protein, gene. ds; incotianamine aminotransferase; plant; iron absorption; iron deficiency chlorosis. Gramineae sp.
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Nicotianamine aminotransferase primer 1.
Ss; nicotianamine aminotransferase; plant; iron absorption; PCR; iron deficiency chlorosis; primer; amplification.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/product= "Nicotianamine aminotransferase"
                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                         V48147 standard; cDNA to mRNA; 1660 BP.
V48147;
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26-Aug-1998.
21-FEB-1998; 102891.
21-FEB-1997; JP-037499.
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MOTI S, NAKANIShi H, Takahashi M; WPI; 98-439341/38.
P-PSDB; W61642.
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Q62115
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Controlling capacitative calcium ion entry into mammalian cells - by changing activity of transient receptor potential proteins, e.g. for treating asthma, hypertension etc.

Treating asthma, hypertension etc.

Claim 12: Page 31-35: 60pp: English.

Claim 12: Page 31-35: 60pp: English.

This cDNA clone codes for a human transient receptor potential

This cDNA clone codes for a human transient receptor potential

CC (Tr) protein (see Wi5961), designated Hrrp3, that is an essential

part of the capacitative calcium ion entry (CCE) mechanism in human

cells. The CDNA was isolated by subjecting human embryo cell line

23 cDNA to RACE-PCR wising primers (see Vi5035-38) based on the

sequence of GeneBank expressed sequence tag EST R3416. Htrp1 (see

Vi5029) cDNA has also been isolated. CCE into a mammalian cell

cypressing a try protein required for CCE is controlled in a

claimed method by treating the cell with an agent that increases or

decreases the amount of blologically active try protein from its

commal level. A gents that inhibit CCE are protein from its

contmal level. A gents that inhibit CCE are protein from its

contmal level. A gents that inhibit CCE are protein from its

contmal level. A gents that inhibit CCE are protein from its

contmal level. A gents that inhibit come are potentially useful for

treating asthma hypertension and osteoporosis, also for

continued method by treating the cell with the cell with the mangement of the cell with the cell with an agent that increases the amount of blologically active try protein from its

contail pathma. Appertension and osteoporosis, also for

contail diabetes and to induce bone formaliation. Primary here
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WPI; 98-230269/20.
Controlling capacitative calcium ion entry into mammalian cells - by changing activity of transient receptor potential proteins, e.g. for Licating asthma, hypertension etc.
Disclosure; Page 9; 60pp; English.
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Htrp3, transient receptor potential, trp protein, human, capacitative calcium ion entry, CCE, asthma; hypertension; diabetes, osteoporosis, osteogenesis, thrombosis, immunodeficiency,
Htrp3; transient receptor potential; trp protein; human;
capacitative calcium ion entry; CCE; asthma; hypertension;
diabetes; osteoporosis; osteogenesis; thrombosis; immunodeficiency;
gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunodeficiency, if associated with trp gene mutations, may treated by gene therapy.

Sequence 3258 BP; 911 A; 720 C; 787 G; 840 T:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 3258;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.8%; Score 15.6; D
65.2%; Pred. No. 29;
cive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene therapy; RACE; PCR; primer; ss. Synthetic.
                                                                                                                           Location/Qualifiers 291. .3080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2502 GACGTGGAGTGGAAGTTTGCAAG 2524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V26038 standard; DNA; 29 BP.
V26038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-MAR-1998.
29-AUG-1997; U15247.
15-OCT-1996; US-729955.
30-AUG-1996; US-025111.
(REGC ) UNIV CALIFORNIA.
                                                                                                                                                                            /*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diabetes; osteoporosis;
                                                                                                                                                                                                                                                                           15-OCT-1996; US-729955.
30-AUG-1996; US-025111.
(REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                    Birnbaumer L, Zhu X;
WPI; 98-230269/20.
P-PSDB; W55961.
                                                                                                                                                                                                                                                    29-AUG-1997; U15247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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W09808979-A1.
                                                                                                         sapiens
                                                                                                                                                                                                        WO9808979-A1
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V26038/c
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Claim 4; Page 14-15; 17pp; English.
The nicotianamine aminotransferase can be used in a plasmid to transform plant cells to produce cells with enhanced iron absorption, and it is implied [though not stated] that plants with improved resistance to iron deficiency chlorosis in calcareous soils can be regenerated from the transformed cells. The gene fragment can be used to detect, amplify and/or isolate nicotianamine aminotransferase genes.
Sequence 1910 BP; 462 A; 534 C; 546 G; 368 T;
                                 Mori S, Nakanishi H, Takahashi M;
Mori S, Nakanishi H, Takahashi M;
MPI; 98-439341/38.

New nicotianamine aminotransferase protein and DNA - useful for
enhancing iron absorption of plant cells
claim 16; Page 7; 17pp; English.

The primers V48149 and V48150 were used in the cloning of nicotianamine
aminotransferase can be used in a plasmid to transform plant cells to
produce cells with enhanced iron absorption, and it is implied [though
not stated] that plants with improved resistance to iron deficiency
chlorosis in calcareous soils can be regenerated from the transformed
cells. The gene fragment can be used to detect, amplify and/or isolate
nicotianamine aminotransferase genes.
Sequence 23 BP; 3 Å; 2 C; 7 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-077-1998 (first entry)
Nicotianamine aminotransferase 58148.62 molecular weight protein, gene.
As; nicotianamine aminotransferase; plant; iron absorption; iron deficiency chlorosis.
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                                                                                                                                                                                                                                                                                                                                                                                                          80.0%; Score 18.4; DB 1; Length 23; 100.0%; Pred. No. 0.46;
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Human transient receptor potential protein Htrp3 cDNA.
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/product= "Nicotianamine transferase"
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100.0%; Preα. ....
'''e 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V48148 standard; cDNA to mRNA; 1910 BP. V48148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-FEB-1997; JP-037499.
(SUMO ) SUMITOMO CHEM CO LTD.
MODI S, MAKANISHI H, TAKAHASHI M;
WPI; 98-419341/38.
P-PSDB; W61643.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  460 GCGGTGGAGTGGAATTTCGCGGG 482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GCNGTNGARTGGAAYTTYGCNMG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 qcngtngartggaayttygcnmg 23
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                  (SUMO ) SUMITOMO CHEM CO LID
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Best Local Similarity 100.
Matches 23; Conservative
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Best Local Similarity
Matches 16; Conserv
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EP-860499-A2.

26-AUG-1998

V26030;

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containing the present invention describes a computer readable medium which has the present invention describes a computer readable medium which has the nucleotide sequences SEO ID NO:1 to 391 (V52134 to V5254) recorded on it, or a representative fragment or a sequence at least 95% identical to SEO ID NO: 1 to 391. The nucleotide sequences depicted in SEO ID NO:1 to 391 (V52134 to V52524) are genomic fragments from Streptococcus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEO ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEO ID NO:1 to 391, identifying members of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the manbers; or (b) isolating meNA, DNA or CDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from the sequence of commercial importance, or expression modulating clasment of the S. pneumoniae genome to prime the amplification modulating fragments of the S. pneumoniae genome. Products from the present compositions and vaccines for S. pneumoniae, or expression modulating fragments of the S. pneumoniae genome. Products from the present compositions and vaccines for S. pneumoniae, or expression modulating fragments of the S. pneumoniae genome. Products from the present compositions and vaccines for S. pneumoniae genome. Products from the present componence in 3073 RPS. S. SACCION S. SAC
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PCR primers S1, S2, A1 and A2 (see V26035-38) are based on the expressed sequence tag EST R34716 from the GenBank dbEST database. They were used in the isolation and identification of Htrp3 cDNA. Primary RACE-PCR amplifications of human embryonic Kidney (HEK) 293 cell cDNA was performed using adaptor primer AP1 in combination. With primers 16 or 3 amplifications of human embryonic Kidney (HEK) 293 cell cDNA was performed using adaptor primer AP1 in combination. Nested-PCR amplifications were performed using internal primers AP2 plus S2 for 3'RACE or AP2 plus A2 for 5'RACE. Positive clones were identified using oligonuclectides A1 and S2 for the Calones were identified using oligonuclectides A1 and S2 for the S2 for a transient receptor potential (trp) protein (see W55051) that is essential for calcium ion entry into cells. The invention relates to methods for treating cells with agents that raise or lower the amount of trp protein and which thereby control capacitative calcium ion entry into the cell, and for using trp proteins as targets for identifying such agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 98-27225/24.
Computer-readable medium with recorded Streptococcus pneumoniae
polynuclootide sequences - useful in diagnostic kits and assays, and
pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae genome fragment SEQ ID NO:115.
Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay;
computer readable medium; vaccine; pharmaceutical composition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3746 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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Barash SC, Choi GH, Dillon PJ, Dougherty BA, Fannon M,
Kunsch CA, Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1558 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.8%; Score 15.6; D
65.2%; Pred. No. 14;
iive 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 gengingariggaayttygenmg 23
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Best Local Similarity 65.2
Matches 15; Conservative
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30-OCT-1997; U19588.
31-OCT-1996; US-029960.
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Sequence 11303 BP;
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2266 C;

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V71710,
V7710,
V7710
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New isolated human uncoupling polypeptide(s) - used to develop products for the diagnosis, prevention and treatment of body weight products for the diagnosis, prevention and treatment of body weight claim 3; Page 24-25, 41pp; English.

This isolated polyunclectide (PN) codes for novel human uncoupling protein HNFCW60 (see W68197). HNFCW60 polynuclectides (see also v54603-04) can be obtained from a CDNA library derived from mRNA in cells of human brain frontal cortex, rhabdomyosarcoma, foetal heart and seeletal muscle using expressed sequence tag analysis. The invention relates to HNFCW60 polypeptides and recombinant materials and methods for their production. It also relates to methods for using such HNFCW60 polypeptides and polynucleotides. Such uses include the treatment of obesity, diabetes, hyperlipidaemia and body weight disorders. The invention also provides methods to identify agonists and antagonists, and methods for treating conditions associated with HNFCW60 imbalance using the identified compounds. In addition, diagnostic assays for detecting diseases asserting associated with inappropriate HNFCW60 activity or levels are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human uncoupling protein HNFCW60 cDNA.
HNFCW60: uncoupling protein; human; body weight disorder; obesity;
diabetes; hyperlipidaemia; diagnosis; therapy; vaccine; ss.
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Length 11303;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                       Indels
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         DB 1;
    Score 15.4; DE
Pred. No. 45;
4; Mismatches
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02
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199. .1137
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                                                                                  4;
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Beeley LJ, Godden RJ, Paine K;
WPI; 98-495841/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               730 CIGIGGAAAGGAACTITGCCC 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      V54602 standard; cDNA; 1193 BP
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    67.0%;
68.4%;
                                                                                                                                                                                                                                                            189 GTCGAATGGAATTTCGCTA 207
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                                                                                                                                                                         4 gtngartggaayttygcnm 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-DEC-1998 (first entry)
    Query Match 67.0°
Best Local Similarity 68.4°
Matches 13; Conservative
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16-JUL-1997; EP-305305.
05-MAR-1997; GB-004551.
18-MAR-1997; GB-005614.
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Best Local Simi
Matches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9839432-A1
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V54602
ID V5
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Flier JS, Lowell BB; WPI; 98-594483/50.
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08-APR-1998; U06959.
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                                                                                                                                                                                                                                                                                                                                                                                                         WO9845438-A1
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V72690
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                                               CDS
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PRESENTINGS: U06959.

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PRESENTINGS: U06959.

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V7711;
V7711;
V7711;
V7711;
V77711;
V77
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/note= reading frame 2; contains internal stop codons
which are not indicated in the corresponding
protein (W81589)"
                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= d
/note= "reading frame 3; contains internal stop codons
which are not indicated in the corresponding
protein (W81590)"
                                                                                                                                                                                             contains internal stop codons
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/note= "reading frame 1; contains internal stop codor
/note= "reading frame 1; contains internal stop codor
protein (W81588)"
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  non-insulin dependent diabetes mellitus; diagnosis; human; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   345 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64.3%; Score 14.8; 161.9%; Pred. No. 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     376 C;
                                                                                                   /*tag= a
/product= "human UCP3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
181. .1008
                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        267 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       V71711 standard; DNA; 1033 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 cngtngartggaayttygcnm 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13; Conservative
                                                                                                                                                                                                                                                                     .1219
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/*tag=
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Best Local Similarity
                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis.
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V71711
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New isolated uncoupling protein, UPP-3 - used to develop products

New isolated uncoupling protein, tissues, e.g. for treating obesity

for modulating thermogenesis in tissues, e.g. for treating obesity

for modulating thermogenesis in tissues, e.g. for treating obesity

PT or muscle wasting caused by infection or cancer

Claim 3; Fig 2A-B; 98pp; English.

CThe invention provides human uncoupling protein 3 short form (UCP3sh).

CThe invention provides human and mouse UCP3 genes (V77170 and V71712)

CThe invention provides human and mouse UCP3 genes (V77170 and be used for identifying compounds which alter UCP3 is involved in

CC or the recombinant production of the protein. The UCP3 is involved in

CC or the regulation of thermogenesis in mammals. The nucleic acids (V77170 can be used for identifying compounds which alter UCP3 activity.

CN 771712) can be used for identifying compounds which alter UCP3 activity.

CN 77172) can be used as anti-obesity drugs. Inhibitors of UCP3 can be used for enhancing protein catabolism in a mammal such as inhibiting

CN 77172) can be used on be used for curtailing muscle wasting the to

CN 77172 can be used for can be used for curtailing muscle wasting due to

CN 77172 can be used on be used for curtailing muscle wasting due to

CN 77172 can be used on be used for curtailing muscle wasting due to

CN 77172 can be used on possible treatment for non-insulin dependent

CN 77172 can be used on possible treatment for non-insulin and

CN 77172 can be used on be used on used for detection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
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Human uncoupling protein UCP3L, UCP3S, oxidative phosphorylation;
Human; uncoupling protein; UCP3L; UCP3S, oxidative phosphorylation;
adenosine triphosphate; mitochondria; skeletal muscle; gene therapy;
thermogenesis; heart; obesity; cachexia; type II diabetes; hypertension;
insulin sensitivity; neuromuscular disease; ss.
Homo sapiens.
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/note= "reading frame 2; contains internal stop codons
which are not indicated in the corresponding
protein (W81593)"
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                                                                                                         /*tag= b
/note= "reading frame 1; contains internal stop codor
which are not indicated in the corresponding
protein (W81592)"
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/*tag= d
/*note= "reading frame 3; contains internal stop codor
/note= "neading frame 3; contains internal stop codor
protein (W81594)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1997; US-892745.
09-APR-1997; US-043447.
12-MAY-1997; US-046254.
(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
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61.9%; Pred. No. 64;
ive 4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; W81591, W81592, W81593, W81594.
/*tag= a
/product= "human UCP3"
1. .1032
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154. .1092
/*tag= a
/product= "UCP3L"
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Best Local Similarity 61.9
Matches 13; Conservative
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WO9852958-A1
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Best Local Simi
Matches 13;
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\mathbb{F}^{3}
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                                                                                                                                                                                                    Firshis Wassist.

Firshis Wassist.

Firshis Wassist.

For treating obsestly and cachexia

Therrive.g. for treating obsestly and cachexia

Therrive.g. for treating obsestly and cachexia

Theresent sequence encodes human uncoupling protein UCP31. UCP3

The present sequence encodes human uncoupling protein UCP31. UCP3

The present sequence encodes human uncoupling protein UCP31. UCP3

Triphosphate in the mitochondria of skeletal muscle. The coding

sequences for UCP31 and UCP3S are useful for gene therapy of

dysfunctions of thermogenesis in human skeletal muscle and heart which

result from a lack of UCP3 and which can induce disorders such as

obesity or cachexia. Antisense oligonucleotides to UCP31 and UCP32 can

be used for correcting an excess of UCP3. Woldification of endogenous

CCP3 activity (using activators or inhibitors of UCP3) is used to induce

bodyweight loss (loss of adipose mass and maintenance of the lean mass)

In all types of obesity by promoting the dissipation of energy; for

configuration accessive weight regain following restrictive food diet or

after ceasing a physical training programme; for preventing and treating

type II diabetes by improving sensitivity to insulin; for preventing

hypertension; for increasing muscle mass in states of cachexia; for

treatment of insufficiencies or disturbances of cardiac rhythm due to a

dysfunction of UCP3; and for the treatment of neuromuscular diseases due

to a dysfunction of UCP3; The uncoupling proteins can also be used to

conserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Human uncoupling protein UCP3S encoding cDNA.

Human; uncoupling protein; UCP3L; UCP3S; oxidative phosphorylation;
adenosine triphosphate; mitochondria; skeletal muscle; gene therapy;
thermogenesis; heart; obesity; cachexia; type II diabetes; hypertension;
insulin sensitivity; neuromuscular disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                generation of transgenic animals, e.g. for screening substances which modify UCP3 expression or activity or for investigating the biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human skeletal muscle uncoupling proteins UCP3L and UCP3S - useful for controlling thermogenesis in human skeletal muscle and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             345 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 14.8; DB
Pred. No. 66;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
DOSS O, Glacobino J, Muzzin P;
WPI; 98-610382/51.
P-PSDB; W83380.
                                                                                         (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
BOSS O, Giacobino J, Muzzin P;
WPI; 98-610382/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          371 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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/*tag= a
/product= "UCP3S"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V72691 standard; cDNA; 1132 BP.
V72691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            685 CTGTGGAAAGGAACTTTGCCC 705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 64.3%;
Best Local Similarity 61.9%;
Matches 13; Conservative
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05-MAY-1998; E02645.
07-MAY-1997; CH-001072.
                       12-NOV-1998.
05-MAY-1998; E02645.
07-MAY-1997; CH-001072.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9850542-A1.
                                                                                                                                                                                        P-PSDB; W8337
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heart, e.g. for treating obesity and cachexia

Claim 3: Page 17-18: 26pp; English.

The present sequence encodes human uncoupling protein UCP3S. UCP3

uncouples oxidative phosphorylation and synthesis of adenosine

triphosphate in the mitochondria of skeletal muscle. The coding

sequences for UCP31 and UCP3S are useful for gene therapy of

dysfunctions of thermogenesis in human skeletal muscle and heart which

result from a lack of UCP3 and which can induce disorders such as

obesity or cachexia. Antisense oligonucleotides to UCP31 and UCP3S can

be used for correcting an excess of UCP3. Modification of endogenous

UCP3 activity (using activators or inhibitors of UCP31 is used to induce

bodyweight loss (loss of adipose mass and maintenance of the lean mass)

in all types of obesity by promoting the dissipation of energy; for

preventing an excessive weight regain following restrictive food diet or

preventing an excessive weight regain following restrictive food diet or

after ceasing a physical training programme; for preventing and treating

type II diabetes by improving sensitivity to insulin; for preventing

type II diabetes by improving sensitivity to insulin; for preventing

type II diabetes by improving sensitivity to insulin; for preventing

dysfunction of UCP3; and for the treatment of neuromuscular diseases due

condition of UCP3; and for the treatment of neuromuscular diseases due

dysfunction of transgente animals, e.g. for screening substances which

condition of transgente animals, e.g. for screening substances which

condition of transgente animals, e.g. for investigating the biological
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26-NOV-1998 ...

26-NOV-1998 ...

26-NOV-1998 ...

26-NOV-1999 ...

20-MAY-1997 ...

20-MAY
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344. .1282
/*tag- /*tag- /*his region is specifically claimed in claim 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 1132;
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Human uncoupling protein 3 (UCP3) cDNA.
Uncoupling protein 3; UCP3; human; obesity; diabetes; hyperinsulinaemia; hypermetabolism; gene therapy; ds.
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1; Mismatches
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61.9%; Pred. No. 65;
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sporozoite;
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The inventors claim a new protein which comprises one or more the inventors claim a new protein which comprises one or more antigence determinants of an Eimeria surface antigen of mol. wt. 28.37,120 or more than 200 kD which specifically binds to one or more monoclonal antibody (MaB) from ATCC HB 9707-9712 (see p93703-6). Also new are DNA encoding the protein (see N92576-9), and a vaccine comprising one or more proteins. Vaccine utility can be enhanced by inserting additional genes into the carrier virus
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
be used for identifying modulators of UCP3 activity. Such modulators can be used for treating diseases such as obesity and diabetes, by manipulating the interrelated process of balancing food intake, energy expenditure and glucose metabolism within the patient. They can also be used to treat hyperactive conditions of energy expenditure which originate in the mitochondria of skeletal muscle. UCP3 nucleic acids are useful in gene therapy of obesity and obesity-related indications, including diabetes, and of mitochondrial-associated hypermetabolism.

Sequence 2340 BP; 606 A; 638 C; 633 G; 463 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N92579/c
ID N92579 standard; DNA; 3094 BP.
AC N92579;
DT 15-MAR-1992 (first entry)
DE Sequence of the 1.7kb cDNA molecule encoding antibodies 7D1,7D4 and 20C6.
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                                                                                                                                                                                                                                                               Score 14.8; DB 1; Length 2340; Pred. No. 73; 4; Mismatches 4; Indels 0
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Eimeria tenella sporozoite 45 kDa surface antigen cDNA.
Coccidiosis, vaccine; poultry; protozoan; parasite; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          796 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA sequences encoding Eimeria surface antigens - used in pox:virus vectors as a vaccine to protect chicks against
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(HOFF ) HOFFMANN-LA ROCHE AG.
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Pred. No. 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262 GCAGGGGAGTGGAAGTTCGCGA 241
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                                                                                                                                                                                                                                                                                                                                                                                 617 A;
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63.6%;
                                                                                                                                                                                                                                                                        64.3%;
61.9%;
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/*tag= a
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Lomedico PT, McAndrew SJ;
WPI; 89-358220/49.
P-PSDB; P93706.
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                                                                                                                                                                                                                                                                                                                   Conservative
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Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP-344808-A.
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T93597/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
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De Co-TUD-1991; US-812349.

PR 20-DEC-1991; US-812349.

RA (HOFF ) HOFFMANN IA ROCHE INC.

Altenburger W, Binger M, Chizzonite RA, Kramer RA,

HOFF ) HOFFMANN IA ROCHE INC.

Altenburger W, Binger M, Chizzonite RA, Kramer RA,

Altenburger W, Binger M, Chizzonite RA, Kramer RA,

Altenburger W, Binger M, Chizzonite RA, Kramer RA,

BI Comedico PT, McAndrew SJ;

RWP1: 97-434379740.

PR WP1: 97-434379740.

PP PSDB; W33624.

PR WP1: 97-804 Sequence comprises the coding region for a 45 kDa protein useful in vaccines to protect poultry against coccidiosis.

Claim 2: Fig 33A-B: 72pp; English.

Claim 2: Fig 33A-B: 72pp; English.

CR CHIS CDNA sequence comprised by monoclonal antibody 7B2

CATCC HB 9712). This antibody also specifically reacts with an Elmeria tenella 200 kDas surface antigen that is present in the correctional antibodies raised against Eimeria antigens. The monoclonal antibodies raised against Eimeria antigens. The containing such DNA sequences (see T93593-98) coding for Eimeria surface antigens (see W31582-84 and W33621-25), recombinant vectors containing such DNA sequences, transformed microorganisms of the transformed microorganisms. Methods are also provided for surface antigens. The surface antigens are also provided containing such proteins or in the form of DNA encoding the proteins in the form of DNA encoding the proteins and viral vector such as a vaccinia virus, other Eimeria species.

Cantinbodies that are cross-reactive with other Eimeria species.
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Eimeria tenella sporozoite 45 kDa surface antigen cDNA.
Coccidiosis, vaccine; poultry; protozoan; parasite; antigen;
sporozoite; ss.
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/note= "base 2001 is given as '8' in Fig20
of the specification"
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.617, aa:Leu)
.620, aa:Ala)
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/transl_except= (pos:603...g)
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AC 193596;
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63.6%;
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26-AUG-1997.
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20-DEC-1991; US-812349.
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Eimeria tenella.
                                                                                                                       US5661015-A.
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Altenburger W, Binger M, Chizzonite RA, Kramer RA,

Altenburger W, Binger M, Chizzonite RA, Kramer RA,

I Comedico PP, McAndrew SJ;

PPSDB; W33621.

New DNA from Eineria tenella and related immunogenic polypeptides -

Probab; Prom Eineria tenella and related immunogenic polypeptides -

This companies to protect poultry against coccidiosis

Claim 1; Fig 20A-D; 72pp; English.

This cDNA clone includes a coding region for a 45 kDa protein (see

W33621) that is recomplised by monoclonal antibody 7B2 (ATC HB 9712).

This antibody also specifically reacts with an Eineria tenella 200

This antibody also specifically reacts with an Eineria tenella 200

This antibody also specifically reacts with an Eineria tenella 200

The surface antigen that is present in the sporozoite developmental

stage. The clone was obtained from a conna limits in munological

screening with monoclonal antibodies raised against Eineria

antigens. The first and last 7 nucleotides of the sequence are

derived from linker sequences used in the cloning procedure. The

chriting such bNA sequences (and in the cloning procedure. The

invention provides DNA sequences (or protecting poultry against conducing the Eineria

surface antigens (see W31582-84 and W33521-26), recombinant vectors

containing such vectors, and methods for producing the Eineria

surface antigens. The surface antigens are administered either as

purified proteins or in the form of DNA encoding the proteins in

surface antigens. The surface antigens are administered either as

purified proteins or in the form of DNA encoding the proteins in

a virall vector such as a vaccinia virus. The vaccines may produce

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a virall vector such say a vaccinia virus, The vaccines may produce
(HOFF ) HOFFMANN LA ROCHE INC.
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Search completed: October 1, 1999, 15:36:18 Job time: 6116 sec g

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Gaps ; 0

Score 14.6; DB 1; Length 3094; Pred. No. 97; 3; Mismatches 5; Indels 0.

Query Match 63.5%; Best Local Similarity 63.6%; Matches 14; Conservative

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October 1, 1999, 15:03:35 ; Search time 1096.08 Seconds (without alignments) 41.391 Million cell updates/sec GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd. 2546578 seqs, 986266752 residues 1 gengtngartggaayttygenmg 23 OM nucleic - nucleic search, using sw model em\_est10:\*
em\_est13:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| criptio       | 50414 0026 | 322 vm13a03.s1 | 311 y 108q05.r | 183 yt87e12 | 744 yx12c12.s | 531 mb47b04.r | 342 mc64e07.r | 228 zd28g09.s | 344 zd60d09.s | 3148 mg51g01. | .0//5 ze22±04. | 16822 zk29b05 | 7664 M193907. | 7000 ZI93009. | 75 mf0/all r | 9678 m175409 | 0109 mi71419 | 1890 m192h08 | 5167 zm86g04. | AA082814 zn25b04.r | 3480 mo24h04. | 2788 zo22d08. | 5601 mr63f03. | 7813 zo48b09. | 1511 Z126h07. | 34/6 MO9/IU3. | 6634 zg80c11 | 2589 mv70b12. | 3010 zr25h03. | 0948 zs06h11. | 9452 va90a06. | 6931 EST41591 | 7651 zw97g04. | 72282 vh0lb03 | 4/4461 VG33609. | 4/344/ VDISALL.<br>5/6082 ************************************ | 521264 01361103. | 521284 aa/500/.<br>555652 wi64201 | 50/8/2 VIO490I. | 640937 0172909 | 64033/ ILL/2603. | Second ing/dos. | 400/6 td09a05. |
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| SUMMA         | AA660      | H11322         | H1391          | H5648       | H9874         | W085          | W4194         | W602          | W76544        | AAOO          | COUCOKK        | AAU3082       | AA05766       | W82322        | W8257        | AA05967      | AA06010      | AA06189      | AA07516       | 8 AA082814         | AA10348       | AA13278       | AA14560       | AA14/81       | 7416247       | AA18799       | AA20663      | AA22258       | AA24301       | AA25094       | AA26945       | AA33693       | AA44 / 00     | AA47448       | 447544          | AA51688  | AA52128          | AASSSSS                           | AA59484         | AA64093        | AA66231          | 100714          | 100*014        |
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## ALIGNMENTS

RESULT 1
AA660414/c
LOCUS
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9D\_est24:\*
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Wilson, R.
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                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophyta; Spermatophyta; Magnollophyta; eudicotyledons; coreeudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
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1 (bases 1 to 539)

Hilliar,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Parsons,J., Hillian,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trewskis,E., Materston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUN-1995
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ym13a03.s1 Soares infant brain 1NIB Homo sapiens CDNA clone
IMAGE:47520 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Long SR
Department of Biological Sciences and Howard Hughes Medical
                                                                                                                                                                        Covitz, P.A., Smith, L.S. and Long, S.R.

Covitz, P.A., Smith, L.S. and Long, S.R.

Expressed sequence tags from a root hair-enriched Medicago truncatula cDNA library

Unpublished (1997)

On Sep 12, 1996 this sequence version replaced gi:1290520.
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Unpublished (1995)
On May 10, 1995 this sequence version replaced gi:805432.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stanford University
Gilbert Biology, Stanford, CA 94305-5020,
121 650 723 323
Frax: 650 725 8309
Email: fa.srl@forsythe.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.0%; Scor.
65.2%; Pred. No. 30,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Institute
                                                                                                                                                        Medicago.
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KEYWORDS
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/uranism="Homo sapiens"
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/db_xref="GDB:420061"
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/clone="Inb="Soares infant brain INIB"
/clone="Inb="Soares infant brain in resistant"
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/dev_stage="73 days post natal"
/dev_stage="73 days post natal"
/dev_stage="73 days post natal"
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I; Site_2: Hin0 III; 1st strand cDNA was primed with a Not
I; Site_2: Hin0 III; 1st strand cDNA was primed with a Not
I; Site_2: Hin0 III; 1st strand cDNA was primed with a Not
I obligo(37) primer [5 double-stranded cDNA was ligated to Hind III adaptors
/double-stranded cDNA was ligated to Hind III adaptors
/entructed constructed with Not I and directionally cloned
into the Not I and Hind III sites of the Lafmid BA vector.
Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."
35 a 132 c 131 g 135 t 6 others
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Washington University School of Medicine
4444 Forcet Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forcet Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1450
High quality sequence stops: 410
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1450 Std Error: 0.00
Seq primer: Promega -2mml3
High quality sequence stop: 410.
Location/Qualifiers
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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yj08905.rl Soares placenta Nb2HP Homo sapiens cDNA clone
IMAGE:148184 5', mRNA sequence.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
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Pred. No. 1.3e+02;
4; Mismatches 4;
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EST.
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Best Local Similarity 63.69
Matches 14, Conservative
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/organism="Homo sapiens"
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/db_xref="GDB:3861301"
/db_xref="Laxon:9606"
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/clone="InAGE:231300"
/clone="InAGE:231300"
/clone="InAGE:231300"
/clone="InAGE:231300"
/clone="InAGE:23100"
/c
Email: est@watson.wustl.edu
Insert Size: 1524
High quality sequence starts: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: polyT not found
Insert Length: 1524 Std Error: 0.00
Seq primer: Prompga -2Iml3
High quality sequence stop: 1.
Location/Qualifiers
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1 (bases 1 to 463)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rikfin,L., Rohlfing,T., Soares,M., Tan,F., Treyaskis,E., Materston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H98744 463 bp mRNA EST 15-DEC-19
yx12c12.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
IMAGE:261526 3', mRNA sequence.
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On Nov 22, 1995 this sequence version replaced gi:1071096
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Faz: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.7%; Score 15.8; DB 23; Length 281; 63.6%; Pred. No. 1.2e+02; Live 4; Mismatches 4; Indels 0;
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H98744.1 GI:1123412
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Matches 14; Conservative
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Hillsor.L. Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J.,
Treyaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
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Genome Res. 6 (9), 807-828 (1996)
Email: estewatson.wustl.edu
Insert Size: 591
High quality sequence stops: 331
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the INAGE Consortium (info@image.llnl.gov) for further information.
Insert Length. 591
Seq primer: MIRR!
High quality sequence stop: 331.
Location/Qualifiers
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Washington University School of Medicine
Washington Daiversity School of Medicine
Tel: 314 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
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                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 15.8; DB 22;
Pred. No. 1.2e+02;
4; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 68.7%;
Best Local Similarity 63.6%;
Matches 14; Conservative
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H56483.1 GI:1005127
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AUTHORS
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GI:1325656
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Best Local Similarity 63.67
Matches 14; Conservative
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 421)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
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WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1012 Std Error: 0.00 seq primer: m13 -40 forward High quality sequence stop: 377.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Nov 29, 1993 this sequence version replaced gi:430122.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                         /organism="Homo sapiens"
/db_xref="GDB:3871168"
/db_xref="taxon:9606"
/clone="IMAGE:261526"
/clone=lib="Soares melanocyte 2NbHM"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 15.8; DB 24;
Pred. No. 1.2e+02;
4; Mismatches 4;
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Source: IMAGE Consortium, LLNL
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Best Local Similarity 63.6%;
Matches 14; Conservative
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Seq primer: ETPrimer
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W08531.1 GI:1282533
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.

1 (Dases 1 to 528)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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Washu-HHMI Mouse EST Project
Mashington University School of MedicineP
4444 Porest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consoitium (info@image.llnl.gov) for further information.
MGI:225116
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Unpublished (1996)
On Apr 14, 1993 this sequence version replaced gi:693673.
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Pred. No. 1.2e+02;
1; Mismatches 4;
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/strain="C57BL/6J"
                                            1. .421
/organism="Mus musculus"
/db_xref="taxon:10090"
/map="1"
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High quality sequence stop: 301.
Location/Qualifiers
High quality sequence stop: 403.
Location/Qualifiers
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63.6%;
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
Email: estewatson.wustl.edu
Email: estewatson.wustl.edu
Email: cono is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1070
Std Error: 0.00
Seq primer: mool.REGA+ET
High quality sequence stop: 414.
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1 (bases 1 to 470)

Hilliar,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Polman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Materston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               zd60009.sl Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone
IMAGE:345041 3', mRNA sequence.
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Unpublished (1995)
On Apr 14, 1993 this sequence version replaced gi:716583.
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 447;
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/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
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/db_xref="GDB:1270416"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/db_sref="taxon:754A01; 12; 12q12-12q13.13"
/clone="IMAGE:345041;
/clone=lib="Soares_fetal_heart_NbHH19W"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Pred. No. 1.2e+02;
4; Mismatches 3;
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/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                  68.7%;
68.2%;
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W76544.1 GI:1386779
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                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 68.7
Best Local Similarity 68.2
Matches 15; Conservative
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AUTHORS
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                                                                               //essue_type="embryo"
//eissue_type="embryo"
//eissue_type="lisisingly"
//ab_host="7910a"
//ab was primed with a Not I - oligo(dT) primer [5'
//ab was primed with a Not I - oligo(dT) primer [5'
//ab was primed with a Not I - oligo(dT) primer [5'
//ab was primed with a Not I and tother and cloned into the Not I and Eco RI sites of the modified primer abonaldo, and was constructed by Bento Soares and M. Fatima Bonaldo. "
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 857 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 405.
Location/Qualifiers
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1 (bases 1 to 447)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rikkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W60228 447 bp mRNA EST 15-OCT-1996 zd28g09.s1 Soares_fetal_heart_NDHH19W Homo sapiens cDNA clone IMAGE:342016 3', mRNA sequence.
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Unpublished (1995)
On Oct 18, 1995 this sequence version replaced gi:1023563.
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                       /clone="IMAGE:353316"
/clone_lib="Soares mouse embryo NbMEl3.5 14.5"
/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 528;
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4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1800
Fax: 314 286 1810
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/db_xref="GDB:1267391"
/db_xref="taxon:9606"
/clone="IMAGE:342016"
/clone_lib="Soares_fetal_heart_NbHH19W"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 15.8; DB 26;
Pred. No. 1.3e+02;
4; Mismatches 4;
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  /db_xref~"taxon:10090'
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134 c 148 g
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| 141 CAGTTGAGGGGAACTTTGCCAG 162
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Best Local Similarity 63.6%;
Matches 14; Conservative
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W60228.1 GI:1366989
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Contact: Wilson RK
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Best Local Similarity 63.6
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Dasea I to 324)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Iacy,M., Le,M., Martin,J., Morris,M., Scheltenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R.

The washu-HMIM Mouse EST Project
Upupblished (1996)

On Nov 4, 1993 this sequence version replaced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pr7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; 1st strand cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washu-HHMI Mouse EST Project
Washington University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
441 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
FhMI: Clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:261896
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA003148 324 bp mRNA EST 19-JUL-1996 mg51g01.rl Soares mouse embryo NbME13.5 14.5 Mus musculus CDNA clone IMAGE:427344 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                            Gaps
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/clone_lib="Soares mouse embryo NDME13.5 14.5"
/sex="unknown"
                                                                                                                                                                                                                                                                       Length 470;
                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH108"
                                                                                                                                                                                                                                                                         Score 15.8; DB 26;
Pred. No. 1.2e+02;
                                                                                                                                                                                                         109 t
                                                                                                                                                                                                                                                                                                            Mismatches
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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High quality sequence stop: 287.
Location/Qualifiers
1. 324
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ilarity 63.6%;
Conservative
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Matches 14; Conserv
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DEFINITION
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JOURNAL
COMMENT
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ORIGIN
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KEYWORDS
SOURCE
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Tel: 314 286 1800
Fax: 314 286 1810
Email: est@atson.wustl.edu
Email: est@atson.wustl.edu
Inhis clone is available royalty-free through LLNL; contact the INAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 697 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA010775 432 bp mRNA EST 29-NOV-1996 ze22f04.rl Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:359743 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is a second of the second
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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On Apr 14, 1993 this sequence version replaced gi:785787.
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/clone="IMAGE:359743"
/clone_l1b="Soares_fetal_heart_NbHH19W"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 15.8; DB 27;
Pred. No. 1.2e+02;
; Mismatches 4;
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/db_xref="GDB:1276287"
/db_xref="taxon:9606"
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Location/Qualifiers
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AA010775.1 GI:1471802
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Length 497;

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68.7%;
63.6%;
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                                                              Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                             house mouse.
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AA038824
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KEYWORDS
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/organism="Homo sapiens"
/db_xref="dDB:3757923"
/db_xref="taxon:9606"
/clone="IMAGE:471921"
/clone="IMAGE:471921"
/clone="IMAGE:471921"
/clone="IMAGE:471921"
/dev_stage="adult"
/dev_stage="adult"
/lab_host="pH108"
/note="Organ: uterus; Vector: pT773-Pac; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I collgo(AT) primer [5/
                                                                                                                                                                                                                                                                                                                                                                                               26-AUG-1996
ZX29b05.rl Scares_pregnant_uterus_NbHPU Homo sapiens cDNA clone
IMAGE:471921 5', mRNA sequence.
4150962
g1509860
AA036822.1 GI:1509860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Wilson RK
Washington University School of Medicine
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Fax: 314 286 1810
Faxi: 315 280 1810
Final: sstewartson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28M13 rev2 from Amersham
High quality: sequence stop: 425.
Location/Qualifilers
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 497)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The WashU-Merck EST Project
Unpublished (1995)
On Apr 14, 1993 this sequence version replaced gi:785518.
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                                                                                                                                                                                                   Score 15.8; DB 27; Length 432;
Pred. No. 1.2e+02;
4; Mismatches 4; Indels 0
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                                                                                                                             105 g
                                                                                                                                                                                                                                       4;
                                                                                                                                                                                                                                                                                          215 CAGTIGAGGGGAACTTTGCCAG 236
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                                                                                                                                                                                                 68.7%;
63.6%;
                                                                                                                             113 c
                                                                                                                                                                                                                                     14; Conservative
                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                      Local
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DEFINITION
                                                                                                                         BASE COUNT
ORIGIN
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JOURNAL
COMMENT
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AUTHORS
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VERSION
KEYWORDS
SOURCE
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Eukaryota; Metazoa, Chordata, Craniata; Vertebrata; Mammalia; Eutheria; Rodentia, Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 360) Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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                                                                                                                                                                                                                                                                                 ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Marra M/Mouse EST Project
WashU-HMIM Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:285140
                                               Gaps
                                                                                                                                                                                                                                          28-AUG-1996
                                                                                                                                                                                                                               AA038824 360 bp mRNA EST 28-AUG-1
mi95g07.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone
IMAGE:474396 5' similar to WP:C28H8.12 CE01823 ;, mRNA sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Waterston,R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Sep 21, 1992 this sequence version replaced gi:276467
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                                          Indels
Score 15.8; DB 27;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seg primer: -28M13 rev2 from Amersham High quality sequence stop: 353. Location/Qualifiers
                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/db_xref="taxon:10090"
/map="8"
                                      4;
                                                                                                   23
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AA038824.1 GI:1514249
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63.6%;
                                                                              2 cngtngartggaayttygcnmg
                                        Conservative
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Best Local Similarity
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mRNA 12-SEP-1996 p3NMF19.5 Mus musculus cDNA clone to WP:C28H8.12 CE01823 ;, mRNA sequence.

12-SEP-1996

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1. .430

/organism="Mus musculus"
/db_rate="Index:0:10013"
/clone="Index:0:10013"
/clone="Index:0:10013"
/clone="Index:0:10013"
/clone="Index:0:10013"
/dev_stage="Index:0:1001"
/dev_stage="Index:0:1001"
/lab_host="DH100 (ammicillin resistant)"
/lab_host="DH100 (ammicillin resistant)"
/lab_host="DH100 (ammicillin resistant)"
/lab_host="Index:0:1001"
/lab_host="Index:0:1
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Marra M/Mouse EST Project
Washington University School of MedicineP
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
444 Fal: 314 286 1800
Fax: 314 286 1810
Fax: 315 286 1810
Fax: 315 286 1810
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Fax: 316 286 1810
Fax: 317 286 1810
Fax: 317 286 1810
Fax: 318 286 1810
Fax: 3
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On Sep 12, 1996 this sequence version replaced gi:1393548.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 393.
Location/Qualifiers
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The WashU-HHMI Mouse EST Project
                                                                                                                 W82322 430 bp
mf04g11.r1 Soares mouse
IMAGE:404132 5' similar
                                                                                                                                                                                                                                                                                                                                  W82322.1 GI:1540001
                                                                                                                                                                                                                                                                                                                                                                                                                            house mouse.
Mus musculus
                                                                                                                                                                                                                                                                                                  q1540001
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/clone_lib="Stratagene corneal stroma (#937222)"
/clone_lib="Stratagene corneal stroma (#937222)"
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/lab_lost="Solne cells (kanamycin resistant)"
/lab_lost="Solne cells (kanamycin resistant)"
/note="Ocran : Cornea; Vector: pBluescript Sk-; Site_l:
EcoRi; Site_l: Xhoi; Clonea udirectionally. Primer:
Oligo dT. Cornea! fibroblasts grown from explants, 76
years. Average insert size: 1.5 kb; Uni-ZAP XR Vector; adaptor sequence: 5; GAATTCGGCACGG 3' -3' adaptor
sequence: 5; GAATTCTGCACAGG 3' -3' adaptor
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2193409.s1 Stratagene corneal stroma (#937222) Homo sapiens CDNA
clone IMAGE:512177 3' similar to TR:G1255188 G1255188 DYNAMITIN. ;,
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Hiller, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Worris, M., Parsons, J., Prange, C., Rifkin, L.,
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J.,
Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Generation and analysis of 280,000 human expressed sequence tags
Genome_Res. 6 (9), 807-828 (1996)
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Washington University School of Medicine
Washington University School of Medicine
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Final: set@wastson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1942 Std Error: 0.00
Seq primer: -40M13 fwd. from Amersham
High quality. sequence stop: 470.
Location/Qualifiers
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    Gaps
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Sep 12, 1996 this sequence version replaced gi:1297673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó;
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Pred. No. 1.3e+02;
1; Mismatches 4; Indels 0
         Indels
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/organism="Homo sapiens'
/db_xref="GDB:3844673"
/db_xref="taxon:9606"
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299 CAGTTGAGGGGAACTTTGCCAG 320
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Best Local Similarity 63.6%;
Matches 14; Conservative
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   Length 430;
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Score 15.8; DB 27;
Pred. No. 1.2e+02;
4; Mismatches 4;
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  68.7%;
63.6%;
                                                                2 cngtngartggaayttygcnmg
   Query Match 68.7
Best Local Similarity 63.6
Matches 14; Conservative
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